LISTING OF CLAIMS

1. ***(currently amended)***: A method for making ~~obtaining~~ a prognosis in a subject of (i) enhanced recovery from an inflammatory condition, ~~[[for]] a subject having,~~ or (ii) increased at risk of developing, the [[an]] inflammatory condition,

the method comprising determining a genotype defined by ~~of said subject at a~~ one or more polymorphic sites in the ~~subject's~~ toll-like receptor 2 (TLR-2) nucleic acid sequence in the subject ~~sequence~~,

wherein said genotype is (a) a protective genotype that is predictive or indicative of an enhanced ability of the subject to recover from the inflammatory condition, or (b) a risk genotype that is predictive or indicative of said increased risk for developing the inflammatory condition.

2. ***(currently amended)***: The method of claim 1, wherein the one or more polymorphic sites includes ~~is at~~ position 201 of SEQ ID NO: 1 or [[at]] a polymorphic site in linkage disequilibrium ~~thereto~~ therewith.

3. ***(currently amended)***: The method of claim 1 ~~any one of claims 1-2~~, further comprising comparing the determined genotype ~~so determined~~ with ~~known~~ genotypes that ~~which~~ are known to be prognostic ~~indicative of a prognosis~~ for recovery from: ~~(i) the subject's type of~~ an inflammatory condition~~; or (ii) another inflammatory condition~~.

4. ***(currently amended)***: The method of claim 1 ~~any one of claims 1-3~~, further comprising ascertaining ~~determining~~ the TLR-2 sequence ~~information for~~ of the subject.

5. ***(currently amended)***: The method of claim 1 ~~any one of claims 1-4~~, wherein said ~~determining of~~ genotype determination is performed on a nucleic acid sample from the subject.

6. ***(currently amended)***: The method of claim 5, further comprising the step of obtaining the [[a]] nucleic acid sample from the subject ~~patient~~.

7. ***(currently amended)***: The method of claim 1 ~~any one of claims 1-6~~, wherein said ~~determining of~~ genotype is determined by ~~comprises~~ one or more of the following methods:

(a) restriction fragment length analysis;
(b) sequencing;
(c) hybridization;
(d) oligonucleotide ligation assay;
(e) ligation rolling circle amplification;

(f) 5' nuclease assay;
(g) polymerase proofreading methods;
(h) allele specific PCR; and
(i) reading sequence data.

8. ***(currently amended)***: The method of claim 1 ~~any one of claims 1-7~~, wherein the risk genotype of the subject is predictive or indicative of (a) decreased likelihood of recovery from [[an]] the inflammatory condition or [[an]] (b) increased risk of having a poor outcome from the inflammatory condition.

9. ***(currently amended)***: The method of claim 8, wherein the subject is critically ill and the presence of the risk genotype is predictive or indicative of ~~a prognosis of~~ severe cardiovascular or respiratory dysfunction.

10. ***(currently amended)***: The method of claim 8 [[or 9]], wherein the risk genotype comprises at least one T nucleotide at position 201 of SEQ ID NO:1.

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12. ***(currently amended)***: The method of claim 1 [[11]], wherein the subject is critically ill and the protective genotype is predictive or indicative of ~~a prognosis of~~ less severe cardiovascular or respiratory dysfunction.

13. ***(currently amended)***: The method of claim 1 ~~11 or 12~~, wherein the protective genotype is defined as homozygosity ~~homozygous~~ for the A nucleotide at position 201 of SEQ ID NO: 1.

14. ***(currently amended)***: The method of claim 1 ~~any one of claims 1-13~~, wherein the inflammatory condition is one that is due to, or associated with, ~~selected from the group consisting of~~: Gram-positive, Gram-negative, culture-negative or fungal sepsis; septicemia; [[,]] septic shock; fever; bacterial viral, fungal or parasitic infection including Group A streptococcus infection; inflammation due to trauma, surgery or a medical or surgical condition associated with increased risk of infection or sepsis; [[,]] pneumonia; [[,]] ~~septic shock,~~ systemic inflammatory response syndrome (SIRS); [[,]] Acute Respiratory Distress Syndrome (ARDS); [[,]] acute lung injury; [[,]] ~~infection~~, pancreatitis; [[,]] bacteremia[[,]] including meningococcemia; [[,]] peritonitis; [[,]] bowel infection; [[,]] abdominal abscess; [[,]] ~~inflammation due to trauma~~, ~~inflammation due to~~ surgery; [[,]] chronic inflammatory disease; [[,]] ischemia; [[,]], ischemia-reperfusion injury ~~of an organ or tissue~~; [[,]] tissue damage due to (i) disease, ~~tissue damage due to~~ (ii) chemotherapy ~~or~~ (iii) radiotherapy, or a ~~and~~ reaction[[s]] to an ingested, inhaled, infused, injected, or delivered substance; [[s,]] glomerulonephritis; [[,]] ~~bowel infection,~~ an opportunistic

infection;~~s, and for patients undergoing major surgery or~~ kidney failure and dialysis; [[,]] immunosuppressive therapy; [[,]] ~~patients who are~~ immunocompromise[[d]] ; [[,]] ~~patients on immunosuppressive agents~~, ~~patients with~~ HIV/AIDS; [[,]] ~~patients with suspected~~ endocarditis; [[,]] ~~patients with fever, patients with fever of unknown origin, patients with~~ cystic fibrosis;~~,~~ ~~patients with~~ diabetes mellitus; ~~, patients with~~ chronic renal failure; ~~, patients with~~ bronchiectasis; ~~, patients with~~ chronic obstructive ~~lung~~ pulmonary disease (COPD); [[,]] chronic bronchitis; [[,]] emphysema; [[~~or~~]]asthma; ~~, patients with~~ febrile neutropenia; ~~, patients with~~ meningitis; ~~, patients with~~ septic arthritis; ~~, patients with~~ urinary tract infection; ~~, patients with~~ necrotizing fasciitis, ~~patients with other suspected Group A streptococcus infection, patients who have had a~~ splenectomy; [[,]]~~, patients with~~ recurrent or suspected enterococcus infection; [[,]]~~, other medical and surgical conditions associated with increased risk of infection, Gram positive sepsis, Gram negative sepsis, culture negative sepsis, fungal sepsis, meningococcemia,~~ post-pump syndrome; [[,]] cardiac stun syndrome; [[,]] myocardial infarction; [[,]] stroke; [[,]] congestive heart failure; [[,]] hepatitis; [[,]] cirrhosis; [[,]] epiglotittis; [[,]] ~~E. coli 0157:H7, malaria,~~ gas gangrene; [[,]] toxic shock syndrome; [[,]] mycobacterial tuberculosis; [[,]] *Pneumocystic carinii* pneumonia; [[,]] Leishmaniasis; [[,]] hemolytic uremic syndrome; [[,]]thrombotic thrombocytopenic purpura; [[,]] Dengue hemorrhagic fever; [[,]] pelvic inflammatory disease ; [[,]] Legionella; [[,]] Lyme disease; [[,]] Influenza A; [[,]] Epstein-Barr virus; [[,]] encephalitis; [[,]] ~~inflammatory diseases and~~ autoimmunity and inflammation due to rheumatoid arthritis, osteoarthritis, or systemic lupus erythematosus; [[,]] inflammatory bowel disease, idiopathic pulmonary fibrosis, sarcoidosis, hypersensitivity pneumonitis, systemic vasculitis, Wegener's granulomatosis; an organ or tissue transplant[[s]] and/or transplant rejection; ~~including heart, liver, lung kidney bone marrow,~~ graft-versus-host disease; ~~, transplant rejection,~~ sickle cell anemia; [[,]] nephrotic syndrome; [[,]] or toxicity caused by monoclonal antibody ~~of agents such as OKT3~~ or cytokine therapy~~, and cirrhosis~~.

15. ***(currently amended)***: The method of claim ~~any one of claims 1~~-14, wherein the inflammatory condition is SIRS.

16. ***(currently amended)***: A method of identifying a polymorphism in a TLR-2 sequence that correlates with or is associated with prognosis of recovery from an inflammatory condition in a subject, the method comprising:

(a) obtaining TLR-2 sequence information from a plurality ~~group~~ of subjects with an inflammatory condition;

(b) based on the sequence information of (a), identifying at least one site of polymorphism ~~polymorphic nucleotide position~~ in the TLR-2 sequence ~~in the subjects~~;

(c) determining [[a]] genotypes defined by said at least one polymorphism ~~at the polymorphic site~~ for individual subjects ~~in the group~~;

(d) determining recovery ability ~~capabilities~~ of individual subjects ~~in the group~~ from the inflammatory condition; and

(e) correlating the genotypes determined in step (c) with the subjects' recovery ~~cap~~abilities determined in step (d),

thereby identifying said ~~TLR-2~~ polymorphisms in said TLR-2 sequence ~~that correlate with recovery~~.

17. ***(currently amended)***: The method of claim 16, wherein the inflammatory condition is one that is due to, or associated with, ~~selected from the group consisting of~~: Gram-positive, Gram-negative, culture-negative or fungal sepsis; septicemia; [[,]] septic shock; fever; bacterial viral, fungal or parasitic infection including Group A streptococcus infection; inflammation due to trauma, surgery or a medical or surgical condition associated with increased risk of infection or sepsis; [[,]] pneumonia; [[,]] ~~septic shock~~, systemic inflammatory response syndrome (SIRS); [[,]] Acute Respiratory Distress Syndrome (ARDS); [[,]] acute lung injury; [[,]] ~~infection~~, pancreatitis; [[,]] bacteremia[[,]] including meningococcemia; [[,]] peritonitis; [[,]] bowel infection; [[,]] abdominal abscess; [[,]] ~~inflammation due to trauma~~, ~~inflammation due to~~ surgery; [[,]] chronic inflammatory disease; [[,]] ischemia; [[,]], ischemia-reperfusion injury ~~of an organ or tissue~~; [[,]] tissue damage due to (i) disease, ~~tissue damage due to~~ (ii) chemotherapy ~~or~~ (iii) radiotherapy, or a ~~and~~ reaction[[s]] to an ingested, inhaled, infused, injected, or delivered substance; [[s,]] glomerulonephritis; [[,]] ~~bowel infection,~~ an opportunistic infection; ~~s, and for patients undergoing major surgery or~~ kidney failure and dialysis; [[,]] immunosuppressive therapy; [[,]] ~~patients who are~~ immunocompromise[[d]] ; [[,]] ~~patients on immunosuppressive agents~~, ~~patients with~~ HIV/AIDS; [[,]] ~~patients with suspected~~ endocarditis; [[,]] ~~patients with fever, patients with fever of unknown origin, patients with~~ cystic fibrosis; ~~, patients with~~ diabetes mellitus; ~~, patients with~~ chronic renal failure; ~~, patients with~~ bronchiectasis; ~~, patients with~~ chronic obstructive ~~lung~~ pulmonary disease (COPD) ; [[,]] chronic bronchitis; [[,]] emphysema; [[~~or~~]]asthma; ~~, patients with~~ febrile neutropenia; ~~, patients with~~ meningitis; ~~, patients with~~ septic arthritis; ~~, patients with~~ urinary tract infection; ~~, patients with~~ necrotizing fasciitis, ~~patients with other suspected Group A streptococcus infection, patients who have had a~~ splenectomy; [[,]]; ~~patients with~~ recurrent or suspected enterococcus infection; [[,]]; ~~other medical and surgical conditions associated with increased risk of infection, Gram positive sepsis, Gram negative sepsis, culture negative sepsis, fungal sepsis, meningococcemia,~~ post-pump syndrome; [[,]] cardiac stun syndrome; [[,]] myocardial infarction; [[,]] stroke; [[,]] congestive heart failure; [[,]] hepatitis; [[,]] cirrhosis; [[,]] epiglotittis; [[,]] ~~E. coli 0157:H7, malaria,~~ gas gangrene; [[,]] toxic shock syndrome; [[,]] mycobacterial tuberculosis; [[,]] *Pneumocystic carinii* pneumonia; [[,]] Leishmaniasis; [[,]] hemolytic uremic syndrome; [[,]]thrombotic thrombocytopenic purpura; [[,]] Dengue hemorrhaigic fever; [[,]] pelvic inflammatory disease ; [[,]] Legionella; [[,]] Lyme disease; [[,]] Influenza A; [[,]] Epstein-Barr virus; [[,]] encephalitis; [[,]] ~~inflammatory diseases and~~ autoimmunity and inflammation due to rheumatoid arthritis, osteoarthritis or systemic lupus erythematosus; [[,]] inflammatory bowel disease, idiopathic pulmonary fibrosis, sarcoidosis,

hypersensitivity pneumonitis, systemic vasculitis, Wegener's granulomatosis; an organ or tissue transplant[[s]] and/or transplant rejection; ~~including heart, liver, lung kidney bone marrow,~~ graft-versus-host disease; ~~, transplant rejection,~~ sickle cell anemia; [[,]] nephrotic syndrome; [[,]] or toxicity caused by monoclonal antibody ~~of agents such as OKT3~~ or cytokine therapy~~, and cirrhosis~~.

18. ***(currently amended)***: A kit useful for determining a genotype of a subject or subjects at a defined polymorphic nucleotide position ~~within a polymorphic site~~ in a TLR-sequence from the subject or subjects, ~~wherein knowledge of the~~ which genotype is associated with ~~provides~~ a prognosis of the subject's ability to recover from an inflammatory condition, the kit comprising;

(a) a restriction enzyme with specificity that distinguishes ~~capable of distinguishing~~ alternate nucleotides at the polymorphic site or sites; or

(b) a labeled oligonucleotide having sufficient complementarity ~~that is sufficiently complementary~~ to an alternate nucleotide sequence at the polymorphic site such that the oligonucleotide hybridizes in a distinguishable manner to a sequence that comprises ~~so as to be capable of specifically hybridizing to~~ said alternate nucleotide sequence, thereby permitting determination of ~~whereby~~ the genotype at [[of]] the polymorphic site ~~may be determined~~; and

(c) optionally, instructions for use of said enzyme and/or said oligonucleotides in determining the genotype.

19. ***(currently amended)***: The kit of claim 18, wherein the polymorphic ~~a polymorphism~~ site is at ~~corresponds to~~ nucleotide position 201 of SEQ ID Noël.

20. ***(currently amended)***: The kit of claim 18 ~~or 19~~ further comprising an oligonucleotide primer or a set of oligonucleotides suitable to amplify a region flanking ~~including~~ the polymorphic site.

21. ***(currently amended)***: The kit of claim 20, further comprising a ~~polymerizing~~ polymerization agent that promotes or permits nucleotide polymerization.

22. ***(currently amended)***: A method for identifying ~~selecting a group of~~ subjects as being suitable for a trial that tests ~~for determining the~~ efficacy of a candidate drug known to be, or suspected of being, useful for treating~~the treatment of~~ an inflammatory disease or condition, the method comprising

(a) determining a genotype defined by ~~for~~ one or more polymorphic sites in the TLR-2 sequence for each of said subjects, wherein said genotype is indicative of

the subject's recovery ability ~~to recover~~ from the inflammatory disease or condition, and

(b) sorting subjects into a suitable and unsuitable group for said trial based on the[[ii]] subjects' genotype.

23. ***(currently amended)***: A ~~The~~ method for testing a candidate drug for its efficacy in the treatment of an inflammatory disease or condition wherein said disease or condition is associated with a genotype defined by a polymorphism in a TLR-2 gene, comprising:

(a) identifying subjects that are suitable for a trial that tests said candidate drug in accordance with of claim 22 ~~further comprising~~; and

(b) administering the candidate drug to [[the]] each of said subjects ~~or a subset of subjects~~, and ~~determining~~ comparing ~~each subject's~~ the subjects' ~~ability to recover from the inflammatory condition~~ responses to said candidate drug in comparison with the subjects' genotype,

thereby testing said candidate drug.

24. ***(currently amended)***: The method of claim 23, wherein a ~~further comprising comparing~~ subject's response to the candidate drug is measured as the ability to recover from the inflammatory condition ~~based on genotype of the subject~~.

25. ***(currently amended)***: The [[A]] method of claim 22 wherein the inflammatory disease or condition is associated with ~~for selecting a group of subjects for determining the efficacy of a candidate drug known or suspected of being useful for the treatment of~~ a gram positive infection~~, the method comprising determining a genotype for one or more polymorphic sites in the TLR-2 sequence for each subject, wherein said genotype is indicative of the subject's likelihood of developing a gram positive infection and sorting subjects based on their genotype~~.

26. ***(currently amended)***: The method of claim 23 [[25]] wherein the inflammatory disease or condition is associated with ~~further comprising, administering the candidate drug to the subjects or a subset of subjects and determining each subject's ability to recover from the~~ a gram positive infection.

27. ***(currently amended)***: The method of claim 24 [[26]], wherein the inflammatory disease or condition is associated with a gram positive infection ~~further comprising comparing subject response to the candidate drug based on genotype of the subject~~.

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40. ***(currently amended)***: The [[A]] method of claim 1 wherein the inflammatory condition is a result of ~~for determining a risk of developing~~ a gram positive infection ~~in a subject, the method comprising determining a genotype of said subject at a polymorphic site in the subject's toll-like receptor 2 (TLR-2) sequence,~~ wherein if said genotype is a risk genotype, it is indicative of the subject's risk of gram positive infection.

41. ***(original)***: The method of claim 40, wherein the polymorphic site is at position 201 of SEQ ID NO:1.

42. ***(currently amended)***: The method ~~any one~~ of claim 40 ~~claims 40-41~~, further comprising ascertaining ~~determining~~ the TLR-2 gene sequence ~~information for~~ of the subject.

43. ***(currently amended)***: The method ~~any one~~ of claim 40, ~~claims 40-42~~, wherein said ~~determining of~~ genotype determination is performed on a nucleic acid sample from the subject.

44. ***(currently amended)***: The method of claim 43, further comprising the step of obtaining [[a]] the nucleic acid sample from the subject~~patient~~.

45. ***(currently amended)***: The method ~~any one~~ of claim 40 ~~claims 40-44~~, wherein said ~~determining of~~ genotype is determined by ~~comprises~~ one or more of the following techniques:

(a) restriction fragment length analysis;
(b) sequencing;
(c) hybridization;
(d) oligonucleotide ligation assay;
(e) ligation rolling circle amplification;
(f) 5' nuclease assay;
(g) polymerase proofreading methods;
(h) allele specific PCR; and
(i) reading sequence data.

46. ***(currently amended)***: The method of claim 40 ~~any one of claims 40-45~~, wherein the risk genotype of the subject is predictive or indicative of the [[a]] subject's risk of developing a gram positive infection.

47. ***(original)***: The method of claim 46, wherein the risk genotype has at least one A nucleotide at position 201 of SEQ ID NO: 1.

48. ***(currently amended)***: The method of claim 46, wherein the protective genotype is defined as homozygosity ~~homozygous~~ for T at position 201 of SEQ ID NO:1.

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52. ***(currently amended)***: An array of nucleic acid molecules immobilized ~~attached~~ to a solid support, the array comprising:

(a) [[an]] a first set of oligonucleotides that

(i) [[will]] hybridize to a nucleic acid molecule consisting of SEQ ID NO:1 in which ~~wherein~~ the nucleotide at position 201 is A, under conditions wherein ~~in which~~

(ii) the oligonucleotides of the first set [[will]] do not substantially hybridize to a nucleic acid molecule consisting of SEQ ID NO:1 in which ~~wherein~~ the nucleotide at position 201 is T; and/or

(b) [[an] a second set of oligonucleotides that

(i) [[will]] hybridize to a nucleic acid molecule consisting of SEQ ID NO: 1, in which ~~wherein~~ the nucleotide at position 201 is T, under conditions wherein ~~in which~~

(ii) the oligonucleotides of the second set will not substantially hybridize to a nucleic acid molecule consisting of SEQ ID NO: 1 in which ~~wherein~~ the nucleotide at position 201 is A.

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